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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/601,168B

DATE: 01/27/2003

TIME: 10:53:49

Input Set : A:\EP.txt

Output Set: N:\CRF4\01242003\I601168B.raw

3 <110> APPLICANT: BENAROUS, Richard  
 4 MARGOTTIN, Florence  
 5 DURAND, Herve  
 6 ARENZANA SEISDEDOS, Fernando  
 7 KROLL, Mathias  
 8 CONDORCET, Jean-Paul  
 10 <120> TITLE OF INVENTION: Human beta-TrCP protein  
 12 <130> FILE REFERENCE: 935.38812X00  
 14 <140> CURRENT APPLICATION NUMBER: US/09/601,168B  
 15 <141> CURRENT FILING DATE: 2000-07-28  
 17 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00196  
 18 <151> PRIOR FILING DATE: 1999-01-29  
 20 <150> PRIOR APPLICATION NUMBER: FR98 01100  
 21 <151> PRIOR FILING DATE: 1998-01-30  
 23 <150> PRIOR APPLICATION NUMBER: FR98 15545  
 24 <151> PRIOR FILING DATE: 1998-12-09  
 26 <160> NUMBER OF SEQ ID NOS: 9  
 28 <170> SOFTWARE: PatentIn Ver. 2.1 and manually  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 2151  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Artificial sequence  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: CDS  
 37 <222> LOCATION: (70)..(1776)  
 39 <220> FEATURE:  
 40 <223> OTHER INFORMATION: Description of the artificial sequence : cDNA  
 41 coding for human beta-TrCP protein  
 43 <400> SEQUENCE: 1  
 44 tgcgttggt gcggcctggc accaaagggg cggccccggc ggagagcgga cccagtggcc 60  
 46 tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111  
 47 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys  
 48 1 5 10  
 50 ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159  
 51 Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro  
 52 15 20 25 30  
 54 agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207  
 55 Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser  
 56 35 40 45  
 58 tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255  
 59 Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr  
 60 50 55 60  
 62 gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303

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63	Ala	Met	Lys	Thr	Glu	Asn	Cys	Val	Ala	Lys	Thr	Lys	Leu	Ala	Asn	Gly	
64			65					70					75				
66	act	tcc	agt	atg	att	gtg	ccc	aag	caa	cgg	aaa	ctc	tca	gca	agc	tat	351
67	Thr	Ser	Ser	Met	Ile	Val	Pro	Lys	Gln	Arg	Lys	Leu	Ser	Ala	Ser	Tyr	
68		80					85					90					
70	gaa	aag	gaa	aag	gaa	ctg	tgt	gtc	aaa	tac	ttt	gag	cag	tgg	tca	gag	399
71	Glu	Lys	Glu	Lys	Glu	Leu	Cys	Val	Lys	Tyr	Phe	Glu	Gln	Trp	Ser	Glu	
72	95					100					105					110	
75	tca	gat	caa	gtg	gaa	ttt	gtg	gaa	cat	ctt	ata	tcc	caa	atg	tgt	cat	447
76	Ser	Asp	Gln	Val	Glu	Phe	Val	Glu	His	Leu	Ile	Ser	Gln	Met	Cys	His	
77				115						120					125		
79	tac	caa	cat	ggg	cac	ata	aac	tcg	tat	ctt	aaa	cct	atg	ttg	cag	aga	495
80	Tyr	Gln	His	Gly	His	Ile	Asn	Ser	Tyr	Leu	Lys	Pro	Met	Leu	Gln	Arg	
81				130					135					140			
83	gat	ttc	ata	act	gct	ctg	cca	gct	cgg	gga	ttg	gat	cat	atc	gct	gag	543
84	Asp	Phe	Ile	Thr	Ala	Leu	Pro	Ala	Arg	Gly	Leu	Asp	His	Ile	Ala	Glu	
85			145					150					155				
87	aac	att	ctg	tca	tac	ctg	gat	gcc	aaa	tca	cta	tgt	gct	gct	gaa	ctt	591
88	Asn	Ile	Leu	Ser	Tyr	Leu	Asp	Ala	Lys	Ser	Leu	Cys	Ala	Ala	Glu	Leu	
89		160				165					170						
91	gtg	tgc	aag	gaa	tgg	tac	cga	gtg	acc	tct	gat	ggc	atg	ctg	tgg	aag	639
92	Val	Cys	Lys	Glu	Trp	Tyr	Arg	Val	Thr	Ser	Asp	Gly	Met	Leu	Trp	Lys	
93	175				180					185					190		
95	aag	ctt	atc	gag	aga	atg	gtc	agg	aca	gat	tct	ctg	tgg	aga	ggc	ctg	687
96	Lys	Leu	Ile	Glu	Arg	Met	Val	Arg	Thr	Asp	Ser	Leu	Trp	Arg	Gly	Leu	
97				195					200					205			
99	gca	gaa	cga	aga	gga	tgg	gga	cag	tat	tta	ttc	aaa	aac	aaa	cct	cct	735
100	Ala	Glu	Arg	Arg	Gly	Trp	Gly	Gln	Tyr	Leu	Phe	Lys	Asn	Lys	Pro	Pro	
101			210					215					220				
103	gac	ggg	aat	gct	cct	ccc	aac	tct	ttt	tat	aga	gca	ctt	tat	cct	aaa	783
104	Asp	Gly	Asn	Ala	Pro	Pro	Asn	Ser	Phe	Tyr	Arg	Ala	Leu	Tyr	Pro	Lys	
105			225					230				235					
107	att	ata	caa	gac	att	gag	aca	ata	gaa	tct	aat	tgg	aga	tgt	gga	aga	831
108	Ile	Ile	Gln	Asp	Ile	Glu	Thr	Ile	Glu	Ser	Asn	Trp	Arg	Cys	Gly	Arg	
109		240				245					250						
111	cat	agt	tta	cag	aga	att	cac	tgc	cga	agt	gaa	aca	agc	aaa	gga	gtt	879
112	His	Ser	Leu	Gln	Arg	Ile	His	Cys	Arg	Ser	Glu	Thr	Ser	Lys	Gly	Val	
113	255				260					265					270		
115	tac	tgt	tta	cag	tat	gat	gat	cag	aaa	ata	gta	agc	ggc	ctt	cga	gac	927
116	Tyr	Cys	Leu	Gln	Tyr	Asp	Asp	Gln	Lys	Ile	Val	Ser	Gly	Leu	Arg	Asp	
117			275					280					285				
119	aac	aca	atc	aag	atc	tgg	gat	aaa	aac	aca	ttg	gaa	tgc	aag	cga	att	975
120	Asn	Thr	Ile	Lys	Ile	Trp	Asp	Lys	Asn	Thr	Leu	Glu	Cys	Lys	Arg	Ile	
121			290					295					300				
123	ctc	aca	ggc	cat	aca	ggt	tca	gtc	ctc	tgt	ctc	cag	tat	gat	gag	aga	1023
124	Leu	Thr	Gly	His	Thr	Gly	Ser	Val	Leu	Cys	Leu	Gln	Tyr	Asp	Glu	Arg	
125			305			310					315						
127	gtg	atc	ata	aca	gga	tca	tcg	gat	tcc	acg	gtc	aga	gtg	tgg	gat	gta	1071
128	Val	Ile	Ile	Thr	Gly	Ser	Ser	Asp	Ser	Thr	Val	Arg	Val	Trp	Asp	Val	

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129      320      325      330
131 aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt 1119
132 Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val
133 335      340      345      350
136 ctg cac ttg cgt ttc aat aat ggc atg atg gtg acc tgc tcc aaa gat 1167
137 Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp
138      355      360      365
140 cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc 1215
141 Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu
142      370      375      380
144 cgg agg gtg ctg gtc gga cac cga gct gct gtc aat gtt gta gac ttt 1263
145 Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe
146      385      390      395
148 gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta 1311
149 Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val
150      400      405      410
152 tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa 1359
153 Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys
154 415      420      425      430
156 cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtg agt ggc 1407
157 Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly
158      435      440      445
160 tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt 1455
161 Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys
162      450      455      460
164 tta cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt 1503
165 Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe
166      465      470      475
168 gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtg 1551
169 Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val
170      480      485      490
172 tgg gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc 1599
173 Trp Asp Leu Val Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu
174 495      500      505      510
176 tgt cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag 1647
177 Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln
178      515      520      525
180 ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc 1695
181 Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu
182      530      535      540
184 atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt 1743
185 Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg
186      545      550      555
188 tcc cct tct cga aca tac acc tac atc tcc aga taaataacca tacactgacc 1796
189 Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
190      560      565
192 tcataacttgc ccaggaccca ttaaagttgc ggtattttaac gtatctgcca ataccaggat 1856
194 gagcaacaac agtaacaatc aaactactgc ccagttttccc tggactagcc gaggagcagg 1916
196 gctttgagac tcctgttggg acacagttgg tctgcagtcg gcccaggacg gtctactcag 1976

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198 cacaactgac tgcttcagtg ctgctatcag aagatgtctt ctatcaattg tgaatgattg 2036
200 gaacttttaa acctccctc ctctcctctt ttacacctg cacctagttt tttcccattg 2096
202 gttccagaca aaggtgactt ataaatatat ttagtgtttt gccagaaaaa aaaaa 2151
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205 <211> LENGTH: 569
206 <212> TYPE: PRT
207 <213> ORGANISM: Artificial sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of the artificial sequence : cDNA
211 coding for human beta-TrCP protein
214 <400> SEQUENCE: 2
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216 1 5 10 15
218 Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
219 20 25 30
221 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
222 35 40 45
224 Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
225 50 55 60
227 Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
228 65 70 75 80
230 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
231 85 90 95
233 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
234 100 105 110
236 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
237 115 120 125
239 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
240 130 135 140
242 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
243 145 150 155 160
245 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
246 165 170 175
248 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
249 180 185 190
251 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
252 195 200 205
254 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
255 210 215 220
257 Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
258 225 230 235 240
260 Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
261 245 250 255
263 Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
264 260 265 270
268 Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
269 275 280 285
271 Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
272 290 295 300

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274 Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
275 305                      310                      315                      320
277 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
278                      325                      330                      335
280 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
281                      340                      345                      350
283 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser
284                      355                      360                      365
286 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
287                      370                      375                      380
289 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
290 385                      390                      395                      400
292 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
293                      405                      410                      415
295 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
296                      420                      425                      430
298 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
299                      435                      440                      445
301 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
302                      450                      455                      460
304 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
305 465                      470                      475                      480
307 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
308                      485                      490                      495
310 Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
311                      500                      505                      510
313 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
314                      515                      520                      525
316 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
317                      530                      535                      540
319 Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro
320 545                      550                      555                      560
322 Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
323                      565
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327 <211> LENGTH: 19
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of the artificial sequence : sense primer
334 <400> SEQUENCE: 3
335 ccaaactgcg tataacgcg
338 <210> SEQ ID NO: 4
339 <211> LENGTH: 20
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: Description of the artificial sequence : antisense primer
346 <400> SEQUENCE: 4

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19

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/601,168B

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Input Set : A:\EP.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 4,5